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# OM protein - protein search, using sw model

Run on: March 1, 2001, 16:22:04 ; Search time 88.16 Seconds  
(without alignments)  
37.226 Million cell updates/sec

Title: US-09-331-631A-32  
Perfect score: 76  
Sequence: 1 CXXCXXCXXXXXXXXXXCXXCXXC 28

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_PHOC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_PODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	72	5 09V199	09v199 drosophila
2	76	100.0	74	5 09V1A1	09v1a1 drosophila
3	76	100.0	152	5 09XVX3	09xvx3 caenorhabd
4	76	100.0	164	5 022048	022048 caenorhabd
5	76	100.0	188	5 018238	018238 caenorhabd
6	76	100.0	413	12 069566	069566 human herpe
7	76	100.0	580	5 09VM37	09vm37 drosophila
8	76	100.0	821	5 09V012	09v012 drosophila
9	76	88.2	46	4 016861	016861 homo sapien
10	67	88.2	58	5 09U623	09u623 pacifastacu
11	67	88.2	104	5 09NLE3	09nle3 leishmania
12	67	88.2	105	5 09NMV2	09nmv2 leishmania
13	67	88.2	108	5 09VUNI	09vuni drosophila
14	67	88.2	110	4 014633	014633 homo sapien
15	67	88.2	115	5 046202	046202 drosophila
16	67	88.2	117	4 095176	095176 homo sapien
17	67	88.2	118	11 002393	002393 mus musculu
18	67	88.2	125	4 095177	095177 homo sapien
19	67	88.2	125	5 09N3Z7	09n3z7 caenorhabd

20	67	88.2	142	5 09U1U5	09u1u5 caenorhabd
21	67	88.2	154	12 084631	084631 paramecium
22	67	88.2	170	6 09TRZ7	09trz7 bos taurus
23	67	88.2	170	6 09TRZ6	09trz6 ovis aries
24	67	88.2	174	5 09ANZ0	09anz0 bombyx mori
25	67	88.2	177	10 09LIU5	09liu5 oryza sativ
26	67	88.2	179	5 09U2J2	09u2j2 caenorhabd
27	67	88.2	188	5 09N8S9	09n8s9 trypanosoma
28	67	88.2	194	4 09U123	09u123 homo sapien
29	67	88.2	194	4 075690	075690 homo sapien
30	67	88.2	212	10 09LNR1	09lnr1 arabidopsis
31	67	88.2	223	11 062220	062220 mus musculu
32	67	88.2	230	11 064507	064507 mus musculu
33	67	88.2	246	4 099750	099750 homo sapien
34	67	88.2	246	4 0991T6	0991t6 homo sapien
35	67	88.2	248	5 096282	096282 plasmodium
36	67	88.2	260	12 084467	084467 paramecium
37	67	88.2	272	2 09S283	09s283 streptomyce
38	67	88.2	273	5 020000	020000 caenorhabd
39	67	88.2	279	12 057148	057148 human herpe
40	67	88.2	315	2 09WX50	09wx50 streptomyce
41	67	88.2	328	5 09TYO1	09tyo1 caenorhabd
42	67	88.2	330	5 018118	018118 caenorhabd
43	67	88.2	341	5 017641	017641 caenorhabd
44	67	88.2	355	4 0991T7	0991t7 homo sapien
45	67	88.2	408	2 083830	083830 treponema p

## ALIGNMENTS

RESULT 1  
ID 09V199 PRELIMINARY: PRT: 72 AA.

AC 09V199: 01-MAY-2000 (TRENBLREL. 13, Created)  
DT 01-MAY-2000 (TRENBLREL. 13, last sequence update)  
DT 01-JUN-2000 (TRENBLREL. 14, last annotation update)  
DE MSTR84DD PROTEIN.  
GN MSTR84DD.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gale R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferliera S., Fleischmann W.,  
RA Fostler A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasio P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003672; AAF54026.1; -  
 DR FLYBASE: FBgn0004173; Mst84db.  
 DR INTERPRO: IPR001450; -  
 DR PROSITE: PS00198; 4FE4S\_FERREDOXIN; UNKNOWN\_2.  
 DR PROSITE: PS00198; 4FE4S\_FERREDOXIN; UNKNOWN\_2.  
 SQ SEQUENCE 72 AA; 6840 MW; BCE374495F88ABA CRC64;

Query Match 100.0%; Score 76; DB 5; Length 72;  
 Best Local Similarity 21.4%; Pred. No. 9.4;  
 Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXCCCCXXXXXCCXCCXCCXCC 28  
 DB 13 CGCGCGCGCGCGCGCGCGCGCGCGCGC 40

RESULT 2  
 ID Q9VIA1 PRELIMINARY; PRT; 74 AA.  
 AC Q9VIA1: 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)  
 DE MSTR84DB PROTEIN.  
 GN MSTR84DB.  
 OS *Drosophila melanogaster* (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Cocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abiril J.F., Abdoyani A., An H.-J., Andrews-Flannock C., Balowin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borotova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mervinov G., Mishina N.V., Modarity C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003672; AAF54024.1; -  
 DR FLYBASE: FBgn0004173; Mst84db.  
 DR INTERPRO: IPR001450; -  
 DR PROSITE: PS00198; 4FE4S\_FERREDOXIN; UNKNOWN\_4.  
 DR PROSITE: PS00198; 4FE4S\_FERREDOXIN; UNKNOWN\_4.  
 SQ SEQUENCE 74 AA; 6725 MW; CC64F0F7A7E7CABC CRC64;

Query Match 100.0%; Score 76; DB 5; Length 74;  
 Best Local Similarity 21.4%; Pred. No. 9.6;  
 Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXXXXCCCCXXXXXCCXCCXCCXCC 28  
 DB 12 CSPCGCGCGCGCGCGCGCGCGCGCGCGC 39

RESULT 3  
 ID Q9YXV3 PRELIMINARY; PRT; 152 AA.  
 AC Q9YXV3: 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)  
 DE C06A1.6 PROTEIN.  
 GN C06A1.6.  
 OS *Caenorhabditis elegans*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditida; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA McMurtry A.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.";  
 RT Submitted (JUN-1995) to the EMBL/Genbank/DBJ databases.  
 RL [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Almscough R., Anderson K., Baynes C., Barks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Lalster N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shonkeen R.,  
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
 RA Thierly-Wieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson C., Weinstein L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.";  
 RT Nature 368:32-38(1994).  
 RL EMBL: Z49886; CAA80055.1; -  
 DR INTERPRO: IPR000561; -  
 DR INTERPRO: IPR001007; -  
 DR INTERPRO: IPR001450; -  
 DR INTERPRO: IPR001502; -  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS00198; 4FE4S\_FERREDOXIN; UNKNOWN\_1.  
 DR PROSITE: PS00764; ENDONUCLEASE\_III\_1; 1.

DR PROSITE: PS01208; VWFC; UNKNOWN\_1.  
SQ SEQUENCE 152 AA; 15645 MW; 6E254F0BE476D354 CRC64;

Query Match 100.0%; Score 76; DB 5; Length 152;  
Best Local Similarity 21.4%; Pred. No. 15;  
Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXC 28  
Db 87 CCTCCRCCTCCCTCCRCCTCCGCCG 114

RESULT 4  
ID Q22048 PRELIMINARY; PRT; 164 AA.  
AC Q22048;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DE T01B7.8 PROTEIN.  
GN T01B7.8.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN 11  
RP SEQUENCE FROM N.A.  
RA Sims M.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.  
RN 12  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
Craighton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,  
Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
Thiery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans.";

RL Nature 368:32-38(1994).  
RT EMBL: Z66499; CA91301.1; -.  
DR INTERPRO: IPR000561; -.  
DR INTERPRO: IPR001007; -.  
DR INTERPRO: IPR001271; -.  
DR INTERPRO: IPR001450; -.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS00198; 4FEAS\_FERREDOXIN; UNKNOWN\_1.  
DR PROSITE: PS00269; DEFENSIN; UNKNOWN\_1.  
DR PROSITE: PS01208; VWFC; UNKNOWN\_1.  
SQ SEQUENCE 164 AA; 16499 MW; C002D48D36C9FCED CRC64;

Query Match 100.0%; Score 76; DB 5; Length 164;  
Best Local Similarity 21.4%; Pred. No. 15;  
Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXC 28  
Db 91 CCCCRCCTCCCTCCCTCCCTCCGCC 118

RESULT 5  
ID Q18238 PRELIMINARY; PRT; 188 AA.  
AC Q18238;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
DE COSMID C27A2.  
GN C27A2.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
Craighton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,  
Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,  
Thiery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
elegans.";

RL Nature 368:32-38(1994).  
RT EMBL: U58760; AAB00710.1; -.  
DR INTERPRO: IPR001007; -.  
DR INTERPRO: IPR001271; -.  
DR INTERPRO: IPR001450; -.  
DR PROSITE: PS00198; 4FEAS\_FERREDOXIN; UNKNOWN\_1.  
DR PROSITE: PS00269; DEFENSIN; 1.  
DR PROSITE: PS01208; VWFC; UNKNOWN\_1.  
SQ SEQUENCE 188 AA; 18678 MW; 0C5D0DC5CABE0C4B CRC64;

Query Match 100.0%; Score 76; DB 5; Length 188;  
Best Local Similarity 21.4%; Pred. No. 17;  
Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXCXXCXXXXXXXXXXCXXC 28  
Db 92 CCCCRCCTCCCTCCCTCCCTCCGCC 119

RESULT 6  
ID Q69566 PRELIMINARY; PRT; 413 AA.  
AC Q69566;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)  
DE (HIV-6) U1102, VARIANT A DNA, COMPLETE VIRION GENOME.  
GN 088.  
OS Human herpesvirus 6.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Roseolovirus.  
OX NCBI\_TaxID=10368;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=U1102, VARIANT A;  
RX MEDLINE=9526321; PubMed=7747482;  
RA Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,  
Marlin M.E., Efstathiou S., Craighton M., Macaulay H.A.;  
RT "The DNA sequence of human herpesvirus-6: structure, coding content,

RT and genome evolution.";  
RL Virology 209:29-51(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=90080132; PubMed=2152817;  
RA Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,  
RT Barrett B.G.;  
RL "Human herpesvirus 6 is closely related to human cytomegalovirus.";  
RN J. Virol. 64:287-299(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=91237802; PubMed=1851860;  
RA Chang C.K., Balachandran N.;  
RT Identification, characterization, and sequence analysis of a cDNA  
RT encoding a phosphoprotein of human herpesvirus 6.";  
RL J. Virol. 65:2884-2894(1991).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=91333007; PubMed=1651403;  
RA Teo I.A., Griffin B.E., Jones M.D.;  
RT "Characterization of the DNA polymerase gene of human herpesvirus 6.";  
RL J. Virol. 65:4670-4680(1991).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=91226542; PubMed=1851252;  
RA Thomson B.J., Efsthathiou S., Honess R.W.;  
RT "Acquisition of the human adeno-associated virus type-2 rep gene by  
RT human herpesvirus type-6.";  
RL Nature 351:78-80(1991).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=91374590; PubMed=1654446;  
RA Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.;  
RT "Identification of a transactivating function mapping to the putative  
RT immediate-early locus of human herpesvirus 6.";  
RL J. Virol. 65:5381-5390(1991).  
RN [7]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=92333249; PubMed=1321206;  
RA Efsthathiou S., Lawrence G.L., Brown C.M., Barrett B.G.;  
RT "Identification of homologues to the human cytomegalovirus US22 gene  
RT family in human herpesvirus 6.";  
RL J. Gen. Virol. 73:1661-1671(1992).  
RN [8]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=92148942; PubMed=1310766;  
RA Geng Y., Chandran B., Josephs S.F., Wood C.;  
RT "Identification and characterization of a human herpesvirus 6 gene 1  
RT promoter.";  
RL J. Virol. 66:1564-1570(1992).  
RN [9]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=93091236; PubMed=1333836;  
RA Gompels U.A., Cars A.L., Sun N., Arrand J.R.;  
RT "Infectivity determinants encoded in a conserved gene block of human  
RT herpesvirus-6.";  
RL DNA Seq. 3:25-39(1992).  
RN [10]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=92260671; PubMed=1374813;  
RA Neipel F., Ellinger K., Fleckenstein B.;  
RT "Gene for the major antigenic structural protein (p100) of human  
RT herpesvirus 6.";

RL J. Virol. 66:3918-3924(1992).  
RN [11]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=92333248; PubMed=1321205;  
RA Thomson B.J., Honess R.W.;  
RT "The right end of the unique region of the genome of human herpesvirus  
RT 6 U102 contains a candidate immediate early gene enhancer and a  
RT homologue of the human cytomegalovirus US22 gene family.";  
RL J. Gen. Virol. 73:1649-1660(1992).  
RN [12]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=93187613; PubMed=8363182;  
RA Ellinger K., Neipel F., Foa-Tomasl L., Campadelli-Piime G.,  
RT Fleckenstein B.;  
RL "The glycoprotein B homologue of human herpesvirus 6.";  
RN J. Gen. Virol. 74:495-500(1993).  
RN [13]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=93224882; PubMed=8385692;  
RA Gompels U.A., Carrigan D.R., Cars A.L., Arno J.;  
RT "Two groups of human herpesvirus 6 identified by sequence analyses of  
RT laboratory strains and variants from Hodgkin's lymphoma and bone  
RT marrow transplant patients.";  
RL J. Gen. Virol. 74:613-622(1993).  
RN [14]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=93389439; PubMed=8397282;  
RA Liu D.X., Gompels U.A., Nicholas J., Leijioft C.;  
RT "Identification and expression of the human herpesvirus 6 glycoprotein  
RT H and interaction with an accessory 40K glycoprotein.";  
RL J. Gen. Virol. 74:1847-1857(1993).  
RN [15]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=94025558; PubMed=7692666;  
RA Liu D.X., Gompels U.A., Foa-Tomasl L., Campadelli-Piime G.;  
RT "Human herpesvirus-6 glycoprotein H and L homologs are components of  
RT the gp100 complex and the gH external domain is the target for  
RT neutralizing monoclonal antibodies.";  
RL Virology 197:12-22(1993).  
RN [16]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=93331710; PubMed=7687803;  
RA Pellett P.E., Sanchez-Martinez D., Dominguez G., Black J.B., Anton E.,  
RA Greenmoyer C., Dambaugh T.R.;  
RT "A strongly immunoreactive virion protein of human herpesvirus 6  
RT variant B strain 229: identification and characterization of the gene  
RT and mapping of a variant-specific monoclonal antibody reactive  
RT epitope.";  
RL Virology 195:521-531(1993).  
RN [17]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=93323202; PubMed=7687301;  
RA Pfeiffer B., Berneman Z.N., Neipel F., Chang C.K., Tiwatnapong S.,  
RA Chandran B.;  
RT "Identification and mapping of the gene encoding the glycoprotein  
RT complex gp82-gp105 of human herpesvirus 6 and mapping of the  
RT neutralizing epitope recognized by monoclonal antibodies.";  
RL J. Virol. 67:4611-4620(1993).  
RN [18]  
RP SEQUENCE FROM N.A.  
RC STRAIN=01102, VARIANT A;  
RX MEDLINE=95146989; PubMed=7844567;  
RA Gompels U.A., Macaulay H.A.;  
RT "Characterization of human telomeric repeat sequences from human  
RT herpesvirus 6 and relationship to replication.";  
RL J. Gen. Virol. 76:451-458(1995).

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RN [19]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=94047392; PubMed=8230490;
RA Dewhurst S., Dollard S.C., Pellett P.E., Damhaugh T.R.;
RT "Identification of a lytic-phase origin of DNA replication in human
RL herpesvirus 6B strain 229."
RN [20]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RA Nicholas J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [21]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=94118404; PubMed=8289364;
RA Nicholas J., Martin M.;
RT "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
RT genome of human herpesvirus 6 encoding human cytomegalovirus
RT immediate-early gene homologs and transactivating functions."
RL J. Virol. 68:597-610(1994).
RN [22]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=94202284; PubMed=8151768;
RA Schiawe U., Neipel F., Schreiner D., Fleckenstein B.;
RT "Structure and transcription of an immediate-early region in the human
RT herpesvirus 6 genome."
RL J. Virol. 68:2878-2985(1994).
RN [23]
RP SEQUENCE FROM N.A.
RC STRAIN=U1102, VARIANT A;
RX MEDLINE=94181269; PubMed=8134119;
RA Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
RA Frenkel N., Rosenthal L.J.;
Query Match 100.0%; Score 76; DB 12; Length 413;
Best Local Similarity 21.4%; Pred. No. 27;
Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXCXXXXXXCXXXXXXCXXXXC 28
DB 298 CILCMSLCMCMCMCMCMCMCMCMCMC 325
RESULT 7
Q9VM37 PRELIMINARY: PRT; 580 AA.
ID Q9VM37
AC 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CG4496 PROTEIN.
GN CG4496.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Borkova D., Botchan M.R., Bouck J., Brokshejn P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
RA Jatali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003616; AAF52490.1; -.
DR HSSP: P07248; IARF.
DR FLYBASE: FBgn0031894; CG4496.
DR INTERPRO: IPR000822; -.
DR PIRAM: PR00096; zf-C2H2; 6.
DR PROSITE: PS00028; ZINC_FINGER_C2H2; 6.
SQ SEQUENCE 580 AA; 66790 MW; 1C038C0D2372B040 CRC64;
Query Match 100.0%; Score 76; DB 5; Length 580;
Best Local Similarity 21.4%; Pred. No. 33;
Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXXCXXCXXXXXXCXXXXXXCXXXXC 28
DB 11 CVDCKCDCTLPCCSASACCDASCDAAAC 38
RESULT 8
Q9VU12 PRELIMINARY: PRT; 821 AA.
ID Q9VU12
AC 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CG17666 PROTEIN.
GN CG17666.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borikova D., Botchan M.A., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durin K.J., Evangelista C.C., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Ferrera S., Fleischmann W.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibeagwa C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Moberly C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman K.S., Pan S., Pollard J., Putl V., Reese M.G.,  
 RA Relter K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spirdling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan W., Zhou X., Zhu S., Zhao Q., Zheng L.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RA "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003540; AAF49882.1; -;  
 DR FLYBASE: FBgn0036311; CG17666.  
 SQ SEQUENCE 821 AA; 89432 MW; 3ABCE80EAD8637FE CRC64;

Query Match 100.0%; Score 76; DB 5; Length 821;  
 Best Local Similarity 21.4%; Pred. No. 41;  
 Matches 6; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXXXXXCCXCCXCC 28  
 DB 669 CMCSCNOCPSMSWYNPCCTCCTTCYCCANC 696

RESULT 9  
 ID 016861 PRELIMINARY; PRT; 46 AA.  
 AC 016861:  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE CYS-1996-1998 (TREMBLrel. 07, Last annotation update)  
 DE CYSTEINE-RICH PROTEIN (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lemasson I., Devaux C., Mesnard J.M.;  
 RL Submitted (Jul-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U63332; AAB05810.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 46 AA; 5061 MW; 311922FE40444E8F CRC64;

Query Match 88.2%; Score 67; DB 4; Length 46;  
 Best Local Similarity 18.5%; Pred. No. 41;  
 Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 2 XXCXXXXXCCCCXXXXXCCXCCXCC 28  
 DB 9 SRCXXXXCCCCCCCCCCCCCCCCCFC 35

RESULT 10  
 ID 090623 PRELIMINARY; PRT; 58 AA.  
 AC 090623:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE METALLOTHIONEIN.  
 OC Pacifastacus lenosculus (Signal crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacoidea; Astacidae; Pacifastacus.  
 OX NCBI\_TaxID=6720;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=THORACIC GANGLIA;  
 RA Skurupski P., Daubart D.;  
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF199482; AAF07215.1; -;  
 DR HSP; P55949; IDMC.  
 DR INTERPRO: IPR002045; -;  
 DR INTERPRO: IPR003019; -;  
 DR PFAM: PF00131; metalhio; 1.  
 DR PRINTS: PR00858; MTCRUSTACEAN.  
 SQ SEQUENCE 58 AA; 6008 MW; 576635ACFBDE5100 CRC64;

Query Match 88.2%; Score 67; DB 5; Length 58;  
 Best Local Similarity 18.5%; Pred. No. 47;  
 Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXCXXXXXCCCCXXXXXCCXCCXCC 27  
 DB 31 CDKCTSGCKCPKBECAKTCSPKRC 57

RESULT 11  
 ID 09NLE3 PRELIMINARY; PRT; 104 AA.  
 AC 09NLE3:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE PROBABLE (HHV-6) U1102, VARIANT A DNA, COMPLETE VIRION GENOME  
 DE (FRAGMENT).  
 GN LM26.499.  
 OS Leishmania major.  
 CC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRIDLIN;  
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivans A.,  
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL160493; CAB98117.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 104 AA; 11240 MW; 0AF0CCD76BB93072 CRC64;

Query Match 88.2%; Score 67; DB 5; Length 104;  
 Best Local Similarity 18.5%; Pred. No. 67;  
 Matches 5; Conservative 22; Mismatches 0; Indels 0; Gaps 0;

OY 2 XXCXXXXXCCCCXXXXXCCXCCXCC 28  
 DB 58 SQCVCCVCCACVCCVCCVCCVCCVCC 84

RESULT 12  
 ID 09NMV2 PRELIMINARY; PRT; 105 AA.  
 AC 09NMV2:



OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxId=7227;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutten G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Modarri C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Splier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=CANTON S; TISSUE=ACCESSORY GLAND; Stelick T.J., Kraus K.W.,  
RA Wolther M.F., Harada H.A., Bertram M.J., Park M., Tram U.,  
RA Kalb J.M., Lung Y.O., Neubaum D.M., Park M., Tram U.,  
RL Insect Biochem. Mol. Biol. 27:0-0(1997).  
DR EMBL: AE003475; AAF47683.1;  
DR EMBL: U85763; AAB9387.1;  
DR FLYBASE: FBgn0020509; Acp62F.  
DR INTERPRO: IPR000561;  
DR INTERPRO: IPR002919;  
DR PFAM: PF01826; TIL; 1.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN.1.  
SQ SEQUENCE 115 AA; 12570 MW; 4326AA6FC32291D CRC64;

Query Match 88.2%; Score 67; DB 5; Length 115;  
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OY 2 XXCXXXXXXCXXXXXXCXXXXXXC 28  
DB 41 TECPVACPETCEYSGNGPCVKMGAPC 67

Search completed: March 1, 2001, 16:22:06  
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